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Research paper

Predicted activity of *UGT2B7*, *ABCB1*, *OPRM1*, and *COMT* using full-gene haplotypes and their association with the *CYP2D6*-inferred metabolizer phenotype

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ABSTRACT

The pharmacogene, *CYP2D6*, is commonly used to infer metabolizer phenotype of many marketed drugs and endogenous toxins in ante- and post-mortem patients but only represents the efficiency of phase 1 metabolism. Downstream metabolic enzymes encoded by *UGT2B7*, *ABCB1*, *OPRM1*, and *COMT* also have been implicated in variable individual response to drugs due to their activity at different stages of the tramadol ADME (absorption, distribution, metabolism, and excretion) process. While commonly studied as single genes using targeted genotyping approaches, a more comprehensive tramadol metabolism profile has not been evaluated. 1000 Genomes Project data for *UGT2B7*, *ABCB1*, *OPRM1*, and *COMT* were used to characterize full-gene haplotypes and their effect on protein function using in-house excel-based workbooks, PopART, and TreeView. Population genetic summary statistics and intergenic analyses associated these haplotypes with full-gene *CYP2D6*-inferred metabolizer phenotype. The findings suggest that *UGT2B7*, *ABCB1*, *OPRM1*, and *COMT* may contribute to predicted metabolizer phenotype as opposed to relying solely on *CYP2D6*.

1. Introduction

The cytochrome p450 family 2, subfamily D, polypeptide 6 (*CYP2D6*) enzyme is responsible for phase I metabolism of approximately 30% of marketed drugs and endogenous toxins [1,2]. *CYP2D6* is a highly variable pharmacogene with well documented allele distributions that vary by demography [3–6]. Constellations of individual single nucleotide (SNPs) or insertion/deletion (INDELs) polymorphisms in *CYP2D6* define star (*) alleles (i.e. a haplotype [operationally defined by a set of SNPs]) which may be used to predict the metabolizer phenotype (e.g. poor [PM], intermediate [IM], extensive/normal [EM/NM] and ultrarapid [UM]) of an individual using their *CYP2D6* diplotype (i.e., combination of two *CYP2D6* * alleles) information and associated activity scores. These data have demonstrated value for guiding individualized prescription medication practices and even post-mortem investigations [7–10].

The *CYP2D6*-inferred metabolizer phenotype describes only one phase of the tramadol (T) ADME (absorption, distribution, metabolism, and excretion) and response process and does not explain all genotypic contribution of an individual's phenotypic expression [11]. Numerous

polymorphisms in the downstream metabolic enzymes uridine diphosphate glucuronosyltransferase, family 1, polypeptide B7 (*UGT2B7*), adenosine triphosphate (ATP) binding cassette, subfamily B, number 1 (*ABCB1*), opioid receptor mu 1 (*OPRM1*), and catechol-O-methyltransferase (*COMT*) also have been implicated in idiosyncratic response to drugs. These ADME proteins are less well characterized and typically are interrogated in single-gene studies that associate relatively few SNPs/INDELs to rate of drug metabolism and/or enzyme activity [12–17]. It has been demonstrated that combinatorial pharmacogenetic profiles (i.e., data from multiple genes) improved patient outcomes in response to antidepressants [18,19] and opiates [20]. Therefore, a higher confidence in predicting a metabolizer phenotype may be realized if information from multiple enzymes in an ADME pathway, such as *CYP2D6*, *UGT2B7*, *ABCB1*, *OPRM1*, and *COMT*, are included in the analysis. For example, a *CYP2D6**4/*CYP2D6**4 homozygote is considered a PM and may be prescribed a higher dose of pro-drug (e.g., T) to reach the therapeutic window. However, that same individual may harbor an *ABCB1* diplotype which confers decreased efflux of O-des-methyltramadol (M1, the primary active metabolite of T) across the blood brain barrier, enabling a relatively large concentration of M1 to

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reach OPRM1 and stimulate analgesia propagation. Ultimately, a patient with this pair of diplotypes at *CYP2D6* and *ABCB1* should experience the desired, and safe, degree of pain relief, but relying solely on *CYP2D6* information for this patient would support increasing the tramadol dose which potentially could cause hyperalgesia.

While combinatorial studies have been performed, they rely on targeted genotyping approaches to interrogate *a priori* SNPs and/or INDELs [13,15,20–24]. Consequently, novel polymorphism(s) cannot be identified that refine estimates of enzyme activity [25]. Massively parallel sequencing (MPS) of the full gene region increases the potential to discover polymorphisms that are currently excluded from phenotype predictions [26].

Herein, the SNP and INDEL variant effect prediction data presented by Wendt et al. [27] are expanded upon using the phased data of the 1000 Genomes Project [28]. Full-gene haplotypes of *UGT2B7*, *ABCB1*, *OPRM1*, and *COMT* were characterized in self-reported healthy individuals. When compared to *CYP2D6*-predicted metabolizer phenotype for the same individuals [25], it was demonstrated that NMs by *CYP2D6* genotyping may possess poorly active downstream metabolic enzymes. Logistic regression suggests that phenotype predictions using *CYP2D6*-inferences alone do not explain all phenotypic variability as there may be contribution from polymorphisms in *UGT2B7*, *ABCB1*, *OPRM1*, and *COMT*.

2. Materials and methods

Polymorphisms in the *UGT2B7*, *ABCB1*, *OPRM1*, and *COMT* gene regions, including introns, exons, 5' and 3' untranslated regions (UTRs), and promoters, were downloaded from Phase 3 of the 1000 Genomes Project and analyzed individually in 5 super- and 26 sub-populations (Table S1) according to Wendt et al. [27]. Haplotypes for each gene were produced according to Table 1 and individual haplotypes are listed in Table S2. Certain polymorphisms characterized were removed from haplotype formation to simplify downstream analyses but capture meaningful levels of variation within each gene. Those excluded variants differ for each gene based on gene size, number of polymorphic sites within each gene, and the consensus variant effect prediction of each polymorphism. In general, polymorphisms that were not scored by Sort Intolerant From Tolerant (SIFT) [34–39], Polymorphisms Phenotyping v2 (PolyPhen-v2) [34,40,41], Protein Variant Effect Analyzer (PROVEAN) [42–44], or Human Splicing Finder (HSF) [45], were removed. Private mutations (SNPs or INDELs) observed once in the 1000 Genomes Project were included/excluded on a gene-by-gene basis. *ABCB1* was divided into four haplotype blocks based on Sai et al. [30,31]. Herein, haplotype block *ABCB1-Block-1* has been extended to include untranslated exon 1 (Fig. 1).

Using in-house Excel-based workbooks, haplotypes were aligned to the hg19 and hg38 reference genomes. Haplotypes were named with the following nomenclature format: reference sequence (genome name)-community recognized star allele (if known)-list of polymorphism rs numbers, if known, and the base at each position. Note that within text haplotypes were referenced using numeric identifiers relative to their frequency in the global population of all 2504 1000 Genomes Project individuals (Table S2).

Population genetic summary statistics for five super- and 26 sub-populations, including haplotype and diplotype frequencies (analogous to allele and genotype frequencies), observed (H_o) and expected (H_e) heterozygosities, pairwise genetic distances, and tests for detection of departures from Hardy Weinberg Equilibrium (HWE) and linkage disequilibrium were performed using Genetic Data Analysis (GDA) [46] and the RStudio® package ggplot2 [47]. TreeView Version 1.6.6 Build 7601 [48,49] was used to create phylogenetic trees; haplotype network analyses were performed using Population Analysis with Reticulate Trees (PopART) using the ancestral parsimony setting [50].

Enzyme activity was predicted using commonly typed and previously described polymorphisms for each gene [13,17,29–31,51–53].

Table 1
Haplotype production approach for *UGT2B7*, *ABCB1*, *OPRM1*, and *COMT*. Private mutations are defined as those observed once in the global population (all 2504 1000 Genomes Project individuals).

Gene	Total Polymorphisms	Full-Gene Haplotypes	Processing Notes	Polymorphisms Removed	Polymorphisms Included	Final Haplotypes
<i>UGT2B7</i>	613	887	Removal of private mutations except those predicted damaging or most likely damaging [27,29]	246	367	641
<i>ABCB1</i>	5986	> 3000	Removal of all unscored polymorphisms [27]; gene broken into haplotype blocks [30,31]	5310	676 Total (51 Block 3; 511 Block 2; 106 Block 1; 8 Block -1)	98 Block 3; 754 Block 2; 208 Block 1; 9 Block -1
<i>OPRM1</i>	6831	> 3000	Removal of all unscored polymorphisms [27]	6627	204	527
<i>COMT</i>	1007	2131	Removal of all unscored polymorphisms [27]	924	83	377

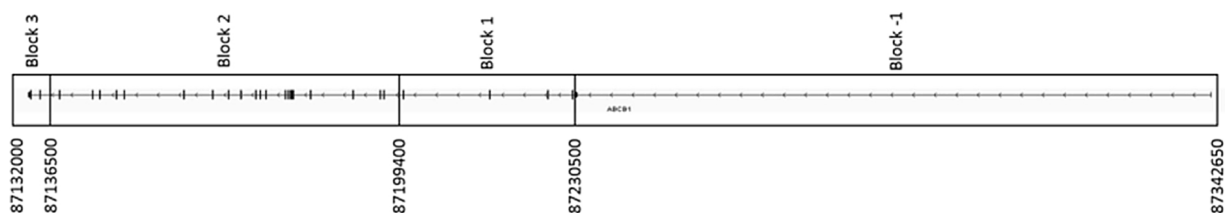


Fig. 1. *ABCB1* haplotype blocks. Image modified from Integrative Genomics Viewer [32,33] indicated chromosome 7 coordinates are relative to the hg19 reference genome.

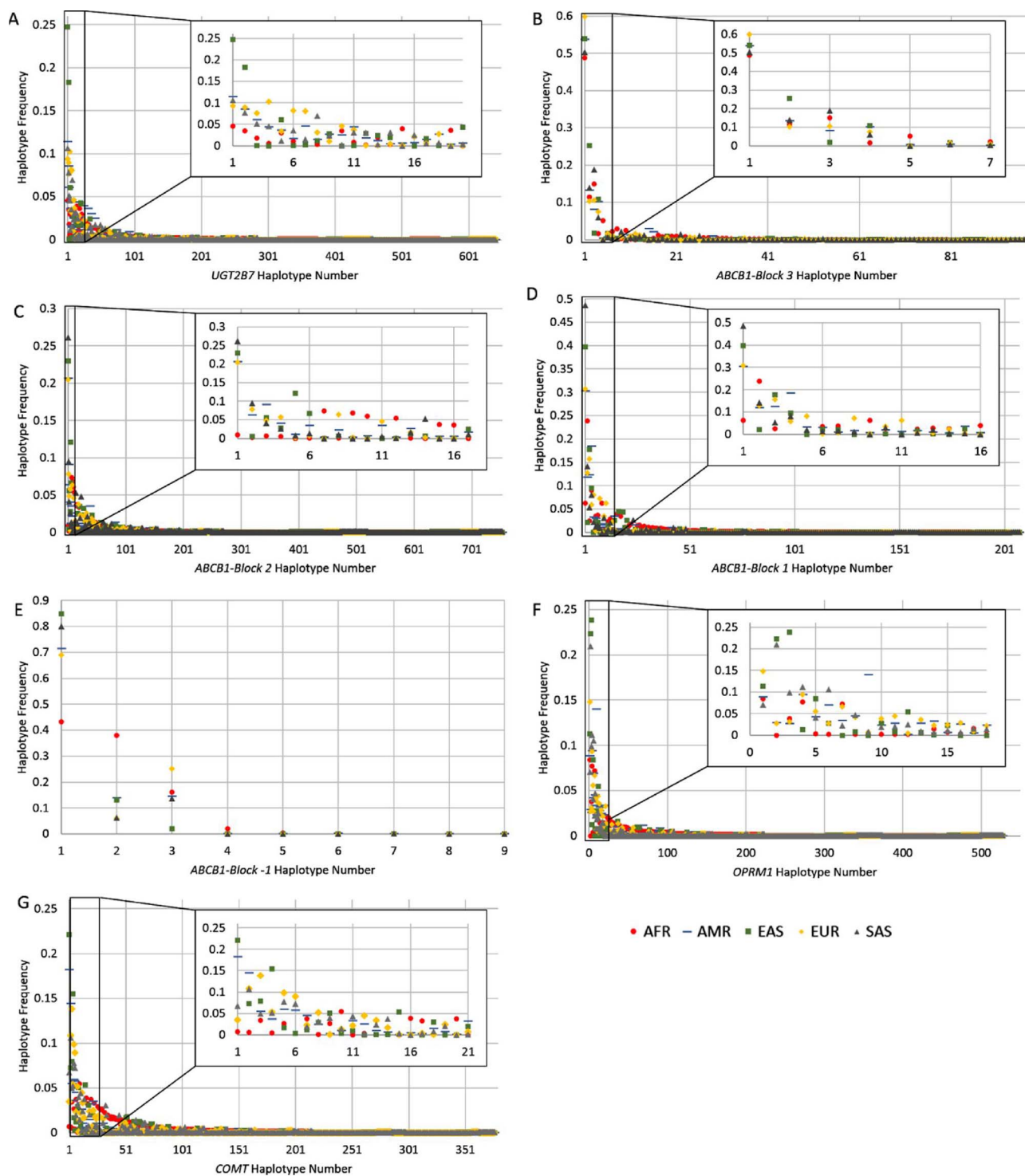


Fig. 2. Haplotype frequencies for *UGT2B7* (A), *ABCB1*-Block 3 (B), *ABCB1*-Block 2 (C), *ABCB1*-Block 1 (D), *ABCB1*-Block -1 (E), *OPRM1* (F), and *COMT* (G) in five super-populations (African [AFR; circles], Admixed American [AMR; horizontal lines], East Asian [EAS; squares], European [EUR; diamonds], and South Asian [SAS; triangles]).

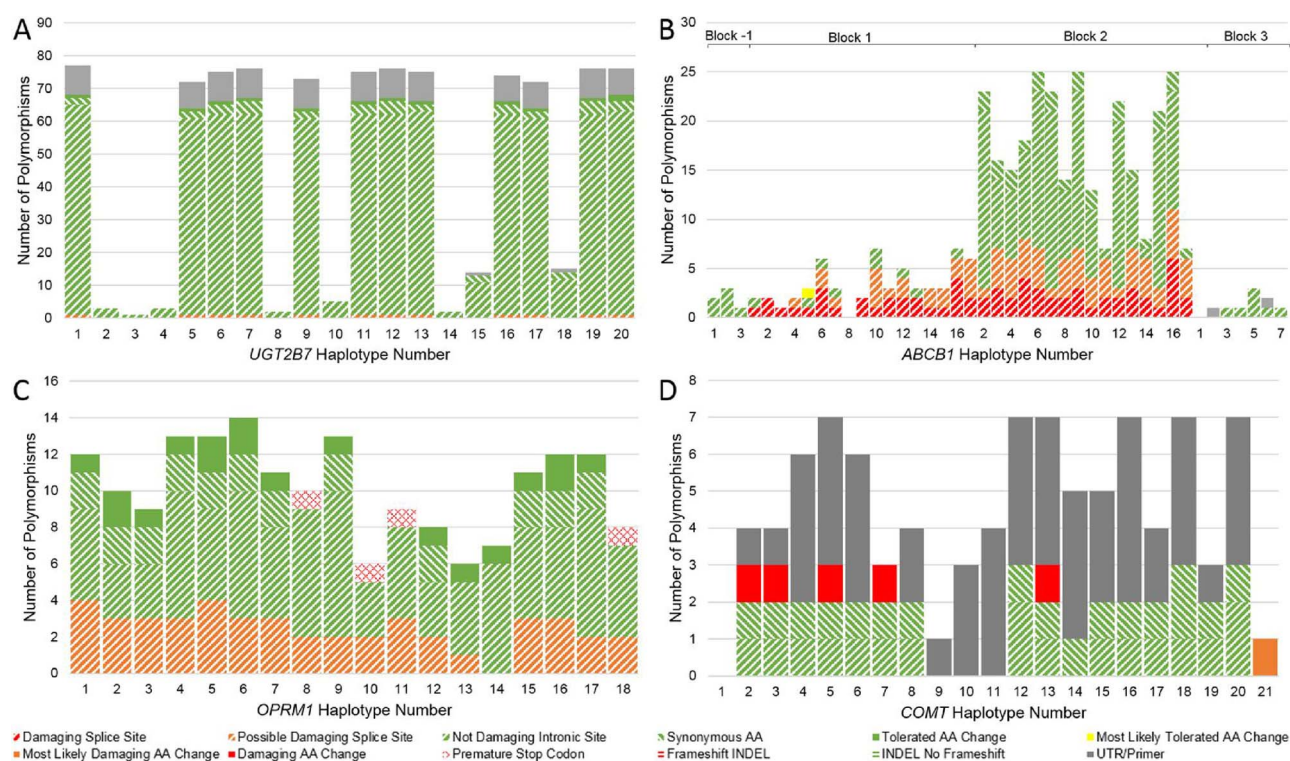


Fig. 3. Haplotype composition of 19, 3, 16, 17, 7, 18, and 21 haplotypes in *UGT2B7* (A), *ABCB1*-Block -1 (B), *ABCB1*-Block 1 (B), *ABCB1*-Block 2 (B), *ABCB1*-Block 3 (B), *OPRM1* (C), and *COMT* (D), respectively, with global frequencies $\geq 1\%$. Variant effect predictions presented by Wendt et al. [27] using Sort Intolerant From Tolerant [34–39], Polymorphism Phenotyping v2 [34,40,41], Protein Variant Effect Analyzer [42–44], and Human Splicing Finder [45].

Due to lack of empirical data for each polymorphism, additional damaging or most likely damaging polymorphisms in a gene were assumed to completely eliminate enzyme function. Logistic regression was used to explore possible relationships between the well-characterized *CYP2D6*-inferred metabolizer phenotype, represented as an activity score (a qualitative measure of phenotype derived from the activity conferred by each * allele an individual carries [54]) and the predicted activity of *UGT2B7*, *ABCB1*, *OPRM1*, and *COMT*. These data were then used to interpret the potential utility of a combinatorial pharmacogenetic profile.

3. Results and discussion

3.1. *UGT2B7*, *ABCB1*, *OPRM1*, and *COMT*

A total of 641, 98, 754, 208, 9, 527, and 377 string sequences were observed for *UGT2B7*, *ABCB1*-Block 3, *ABCB1*-Block 2, *ABCB1*-Block 1, *ABCB1*-Block -1, *OPRM1*, and *COMT*, respectively (Table 1 and Fig. 2). *ABCB1*-Block 3 haplotype 1, *ABCB1*-Block 2 haplotype 191, *ABCB1*-Block 1 haplotype 8, *ABCB1*-Block -1 haplotype 3, and *COMT* haplotype 1, respectively, were identical to the hg19/hg38 reference genomes. No *UGT2B7* and *OPRM1* haplotypes were identical to the hg19/hg38 reference sequences. A majority of haplotypes were observed once in the global population so the average global frequency of haplotypes for each gene was quite low (0.00156 ± 0.00690 for *UGT2B7*, 0.0102 ± 0.0566 for *ABCB1*-Block 3, 0.00133 ± 0.00699 for *ABCB1*-Block 2, 0.00481 ± 0.0243 for *ABCB1*-Block 1, 0.111 ± 0.222 for *ABCB1*-Block -1, 0.00190 ± 0.00873 for *OPRM1*, and 0.00265 ± 0.00900 for *COMT*). *UGT2B7* haplotypes 1–20, *ABCB1*-Block 3 haplotypes 1–7, *ABCB1*-Block 2 haplotypes 1–17, *ABCB1*-Block 1 haplotypes 1–16, *ABCB1*-Block -1 haplotypes 1–3, *OPRM1* haplotypes 1–18, and *COMT* haplotypes 1–21 had global allele frequencies $\geq 1\%$ (Fig. 2), with average frequencies of 0.0284 ± 0.0278 for *UGT2B7*, 0.127 ± 0.186 for *ABCB1*-Block 3, 0.0293 ± 0.0371 for *ABCB1*-Block

2, 0.0516 ± 0.0748 for *ABCB1*-Block 1, 0.331 ± 0.229 for *ABCB1*-Block -1, 0.0371 ± 0.0311 for *OPRM1*, and 0.0298 ± 0.0255 for *COMT*.

Variant compositions for the most common haplotypes of each gene and for all haplotypes are displayed in Figs. 3 and S1, respectively. Empirical data are not present for the large number of haplotypes observed so for the descriptive purposes of this work, the presence of one damaging, or most likely damaging [27,34–45], polymorphism in the haplotype is considered sufficient to decrease enzyme function. The average number of polymorphisms per haplotype was 59.8 ± 27.6 for *UGT2B7*, 3.56 ± 1.01 for *ABCB1*-Block -1, 4.50 ± 1.97 for *ABCB1*-Block 1, 16.5 ± 7.00 for *ABCB1*-Block 2, 3.08 ± 1.21 for *ABCB1*-Block 3, 11.3 ± 2.62 for *OPRM1*, and 4.89 ± 1.99 for *COMT*. Due to limited studies of the polymorphic nature of these four genes and inclusion of additional interrogated regions, none of the observed sequences herein were identical to previously reported star (*) alleles (a haplotype of polymorphisms along the length of the gene region) for *UGT2B7*, *ABCB1*, *OPRM1*, and *COMT*. It should be noted that a substantial number of SNPs/INDELs found in each haplotype (Figs. 3 and S1) are found in intronic or 5' and 3' untranslated regions and may have no individual impact on protein function but may play roles in regulating splice variation, rate of transcription, or have epistatic effects.

Network analysis was performed to determine the relatedness of two sets of haplotypes for each gene of interest: (1) haplotypes having $> 1\%$ global haplotype frequency (Fig. 4), and (2) haplotypes observed more than once in the 1000 Genomes Project dataset (Fig. S2). Networks for *UGT2B7*, *ABCB1*-Block 3, *ABCB1*-Block 2, and *ABCB1*-Block 1 haplotypes (Fig. S2) appear to have more clearly defined haplotype relationships, less looping (multiple haplotypes may have multiple relationships with nearby haplotypes), and/or less reticulation (the degree of “webbing” in the network) than those of *OPRM1* and *COMT*. This observation is possibly attributable to the relatively few number of polymorphisms separating *OPRM1* and *COMT* haplotypes or be an artifact of deleting private mutations which may sufficiently

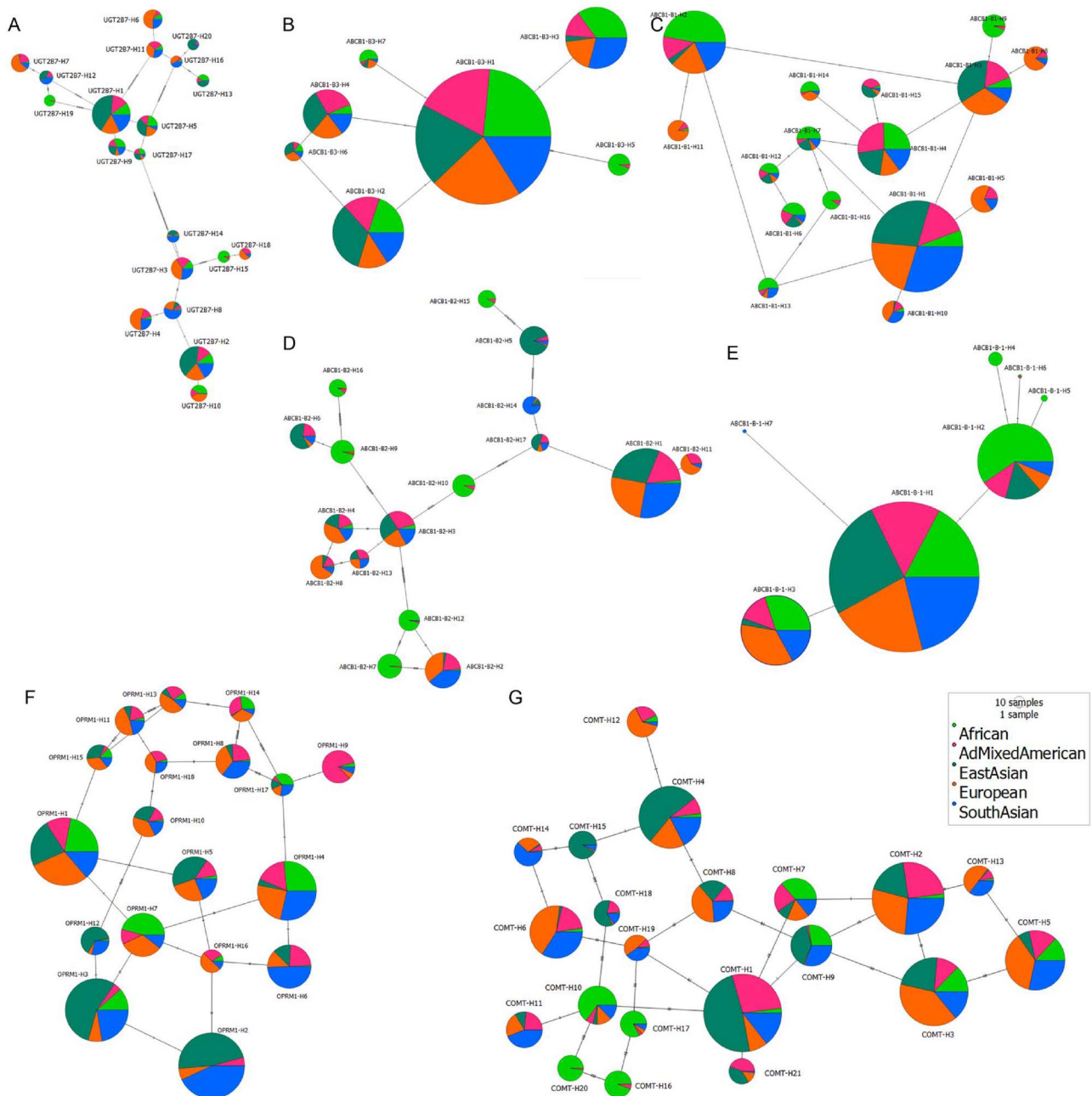


Fig. 4. Network analysis of *UGT2B7* haplotypes 1–20 (A), *ABCB1*-Block 3 haplotypes 1–7 (B), *ABCB1*-Block 2 haplotypes 1–17 (C), *ABCB1*-Block 1 haplotypes 1–16 (D), *ABCB1*-Block -1 haplotypes 1–9 (E), *OPRM1* haplotypes 1–18 (F), and *COMT* haplotypes 1–21 (G). The size of each circle is proportional to the global frequency of each haplotype, segments within each circle are proportional to the super-population haplotype frequency, and lines connecting circles are dashed with the number of mutations separating two haplotypes.

differentiate the relationships between haplotypes; alternatively, the substantial reticulation in the *OPRM1* and *COMT* haplotype networks might also suggest some degree of recombination between the regions of interest. Most major haplotypes in all four genes were observed in all five super-populations while many minor haplotypes were unique to one super-population, namely African (i.e., *UGT2B7* haplotypes stemming from *UGT2B7*-H19). This observation may be due to population-specificity and/or sampling effects.

There were 1414, 225, 1530, 567, 17, 1219, and 1267 unique *UGT2B7*, *ABCB1*-Block 3, *ABCB1*-Block 2, *ABCB1*-Block 1, *ABCB1*-Block -1, *OPRM1*, and *COMT* diplotypes, respectively, observed across 2504 individuals. The average global diplotype frequencies were $7.07 \times 10^{-4} \pm 0.00151$ for *UGT2B7*, 0.00444 ± 0.0234 for *ABCB1*-Block 3, $6.534 \times 10^{-4} \pm 0.00149$ for *ABCB1*-Block 2, 0.00176 ± 0.00685 for *ABCB1*-Block 1, 0.0588 ± 0.125 for *ABCB1*-

Block -1, $8.20 \times 10^{-4} \pm 0.00211$ for *OPRM1*, and $7.96 \times 10^{-4} \pm 0.00142$ for *COMT*. Population-specific diplotype frequencies are displayed in Fig. S5. The average observed diplotype heterozygosity was 0.850 ± 0.129 , 0.745 ± 0.172 , 0.690 ± 0.224 , 0.753 ± 0.170 , 0.687 ± 0.191 for the African (AFR), Ad Mixed American (AMR), East Asian (EAS), European (EUR), and South Asian (SAS) super-populations, respectively. Prior to Bonferroni correction ($p < 0.05$), *UGT2B7*, *OPRM1*, and *COMT* deviated significantly from HWE expectations in all five, two (AFR and EAS), and one (AMR) super-populations, respectively. After Bonferroni correction ($p < 0.00714$), *UGT2B7* and *OPRM1* deviated significantly from HWE expectations in four (AMR, EAS, EUR, and SAS) and one (EAS) super-populations, respectively, out of the five total super-populations (Fig. 5).

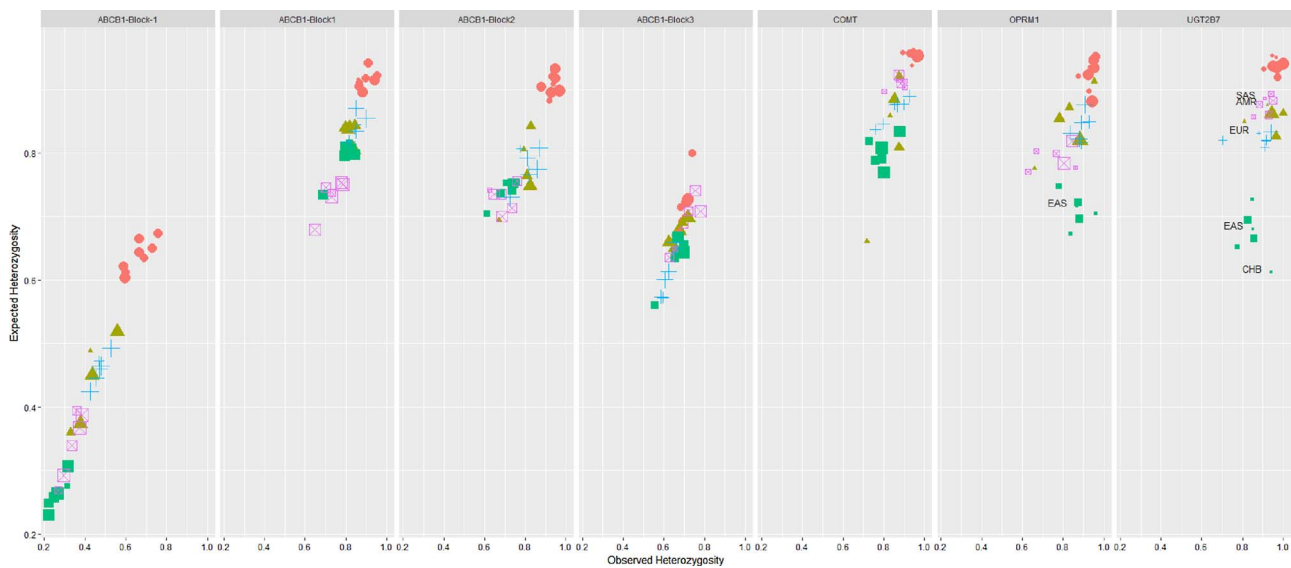


Fig. 5. Observed and expected heterozygosity of *ABCB1*-Block -1, *ABCB1*-Block 1, *ABCB1*-Block 2, *ABCB1*-Block 3, *COMT*, *OPRM1*, and *UGT2B7* haplotypes in five super-populations (African [AFR] in solid circles; Admixed American [AMR] in solid triangles; East Asian [EAS] in squares; European [EUR] in plus signs; South Asian [SAS] in “X”-filled squares) and the 26 sub-populations within each super-population. The size of each data point represents the Hardy-Weinberg Equilibrium p-value for each population; labeled populations indicate significance after Bonferroni correction ($p < 0.00714$).

3.2. Intergenic analyses

Unrooted neighbor-joining trees (Fig. S4) of super- and sub-populations using each gene individually (*ABCB1* is a combination of all four haplotype blocks) tend to show separation more so of the AFR and EAS populations while the AMR, EAS, and SAS populations cluster closer together. Considering all five genes (Fig. 6) the same super-population trend is seen. Generally, the sub-populations within each super-population were grouped closely together; however, the Gujarati Indian from Houston, Texas (GIH) and the Peruvians from Lima, Peru (PEL) populations plot separately from the group of AMR, EUR, and SAS sub-populations.

Intergenic pairwise LD was tested using full-gene haplotypes for *CYP2D6* [25], *UGT2B7*, *ABCB1*-Block 3, *ABCB1*-Block 2, *ABCB1*-Block 1, *ABCB1*-Block -1, *OPRM1*, and *COMT* to identify associations between metabolically relevant genes. Prior to Bonferroni correction ($p < 0.05$) and after removal of significant associations between *ABCB1* haplotype blocks, there were ten, 16, eight, five, and ten significant pairwise LDs in the AFR, AMR, EAS, EUR, and SAS super-populations, respectively (Fig. 7 Figs. 7 and S5). After Bonferroni correction ($p < 0.00179$), there were six, five, one, two, and one significant pairwise LDs in the AFR, AMR, EAS, EUR, and SAS super-populations, respectively, most of which contain *CYP2D6* and an additional downstream metabolic enzyme. The AFR super-population exhibited more LDs than any other super-population (though the significant correlations are weak [average Pearson's $r = 0.0181$]) and those increased LDs are detected in the AFR sub-populations as well. These data are contrary to the expectations of lower LD in AFR populations compared with other population groups [55] but were observed with the individual SNP data as well so this observation is not surprising [27]. However, the effect may be artifactual and possibly explained by the highly polymorphic nature of these genes in the AFR population which results in an overall low frequency of each haplotype (Fig. 2). Consequently, a large number of diplotypes may be observed only once in the AFR super-population, making the comprised haplotypes appear to be in LD due to scant observations of each haplotype. When compressed to minimize the impact of rare diplotypes using the “collapse less-frequent alleles” function in GDA, significant LDs were observed between *CYP2D6* and *UGT2B7*, *ABCB1*-Block -1, *ABCB1*-Block 1, *ABCB1*-Block 2, *ABCB1*-Block 3, *OPRM1* and *COMT*, with Pearson's r -values ranging from -0.0562 to

0.0610 for AFR and -0.0903 to 0.129 for AMR. Though not observed across the whole ADME process, there were some significant LDs between *CYP2D6* and other downstream enzymes in the EAS, EUR, and SAS populations as well. Of particular interest are the significant pairwise LDs between *CYP2D6*/*UGT2B7* (-0.0562 [AFR] to 0.0934 [AMR]) and *CYP2D6*/*COMT* (-0.0902 [EUR] to 0.129 [AMR]) in all five super-populations, which may represent associations between their functional impact. The *COMT* locus is found in a one megabase (Mb) region of chromosome 22 with a relatively high average recombination rate (2.40 ± 1.56 centimorgans/Mb) which may artificially inflate the LD pattern involving this locus [55–59]. These empirical data have not yet been explored and more research is needed to support whether an effect is real.

Using previously identified genotype-phenotype data [13,17,29–31,51–53] and additional polymorphisms characterized by Wendt et al. [27], the activities of *UGT2B7*, *ABCB1*, *OPRM1* and *COMT* were predicted for each 1000 Genomes Project individual. When grouped by *CYP2D6*-inferred metabolizer phenotype as a global cohort (2504 self-reported healthy individuals), there was no association detected between metabolizer phenotype and the diplotype-predicted activity of the selected downstream metabolically-relevant enzymes. Positive and negative correlations were observed between *COMT* ($p = 0.0223$) and *UGT2B7* ($p = 0.0389$) and *CYP2D6* activities, respectively; however the variance at *CYP2D6* activity score of 3 is quite large and may have influenced the significance of this relationship (Fig. 8A shaded regions). *CYP2D6* activity score of 3 was only detected in one Toscani in Italia individual who carries one normally active and one increased activity *CYP2D6* * allele (*CYP2D6**1/*53). On the super-population level, there were more obvious trends, again between *UGT2B7* and *COMT* activities and the *CYP2D6* activity score. Two super-populations showed significant associations between *CYP2D6* and other enzyme activity: AMR and *UGT2B7* ($p = 0.0340$), and EAS and *OPRM1* ($p = 0.0361$). The remaining super-populations and genes did not exhibit significant associations between the *CYP2D6*-inferred metabolizer phenotype and diplotype-predicted downstream metabolic activity. Variant effect predictions [34–45] suggested that all 1000 Genomes Project self-reported healthy individuals possess an *ABCB1* diplotype that confers abnormal transporter activity. This observation may be misleading due to inaccuracies of the variant effect prediction programs used [27]. The functional consequences of individual *ABCB1*

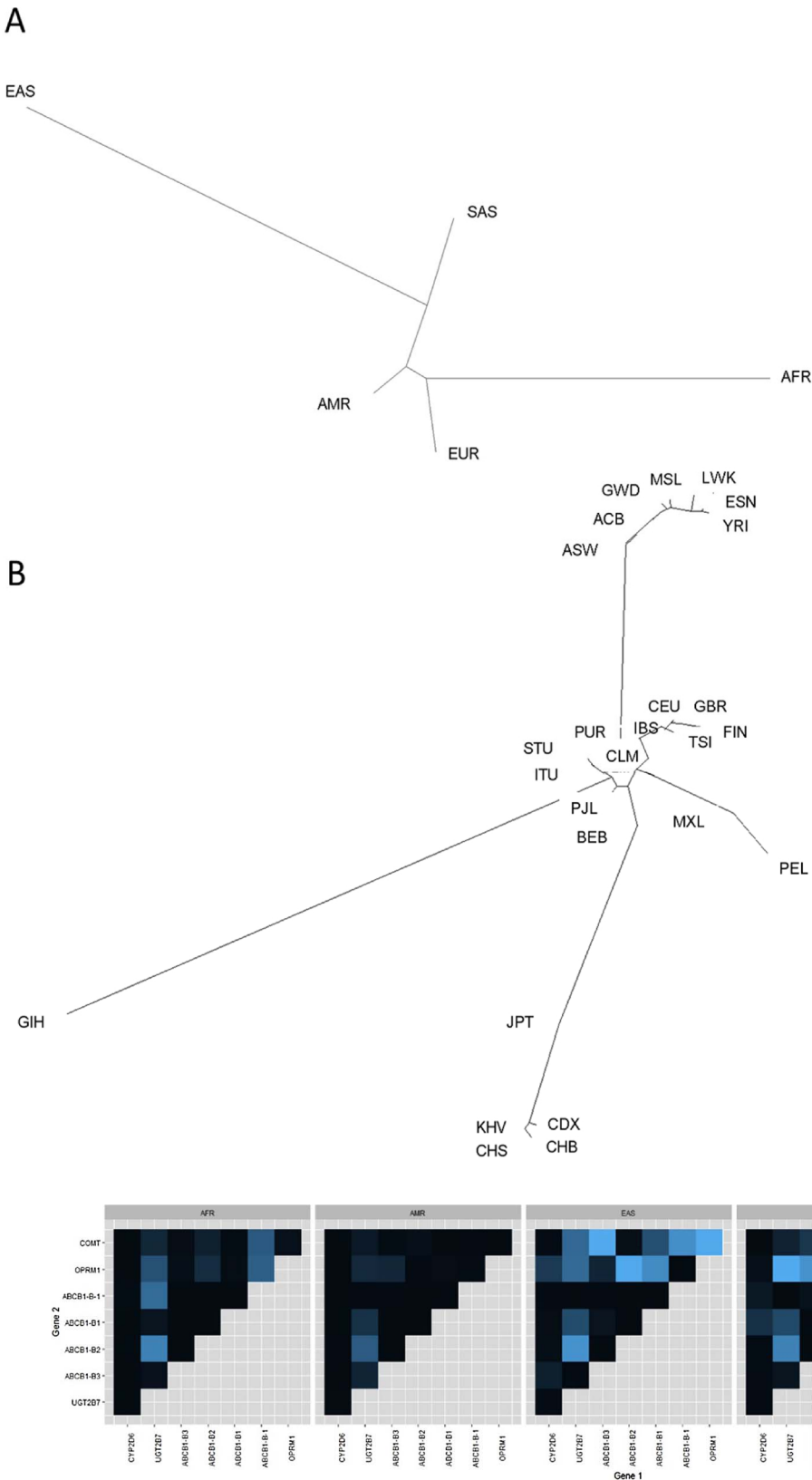


Fig. 6. Neighbor-joining trees for five super- (A) and twenty-six sub-populations (B) in the 1000 Genomes Project using pairwise genetic distances based on *CYP2D6* [25], *UGT2B7*, *ABCB1-Block 3*, *ABCB1-Block 2*, *ABCB1-Block 1*, *ABCB1-Block -1*, *OPRM1*, and *COMT* haplotype assignments.

Fig. 7. Heat maps of pairwise linkage disequilibrium p-values using *CYP2D6* [25], *UGT2B7*, *ABCB1-Block 3*, *ABCB1-Block 2*, *ABCB1-Block 1*, *ABCB1-Block -1*, *OPRM1*, and *COMT* diplotype in the African (AFR), Admixed American (AMR), East Asian (EAS), European (EUR), and South Asian (SAS) super-populations.

polymorphisms, the combined impact of multiple *ABCB1* polymorphisms, and the interaction between the effects of multiple polymorphisms in different genes are unavailable for comparison in this study but eventually will be needed to be empirically evaluated in affected, or

drug-exposed, populations. If these observations are correct, the relative abundance of these splice-altering polymorphisms suggests that decreased ATP-dependent efflux efficiency may be the norm for self-reported healthy individuals. For example, rs2235027 has an alternate

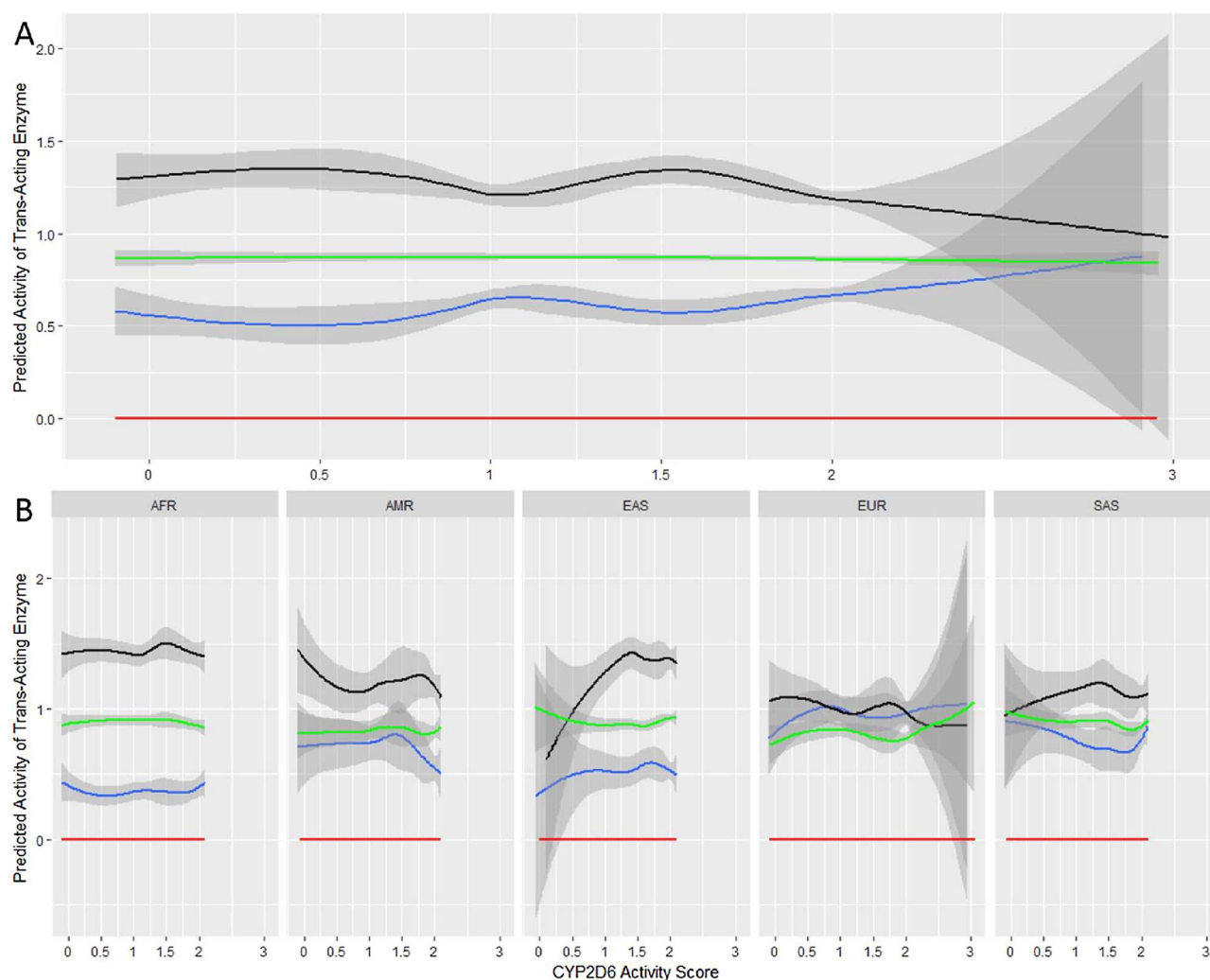


Fig. 8. Regression analysis between CYP2D6 metabolizer phenotype [25] and predicted activity of downstream metabolic enzymes *UGT2B7* (blue), *ABCB1* (red), *OPRM1* (green), and *COMT* (black) in the global population of 2504 1000 Genomes Project individuals (A) and by super-populations (B). Predicted activity of each trans-acting metabolic enzyme is based on the sum of predicted haplotype activities and ranges from zero to two (inactive to normally active, respectively). (For interpretation of the references to color in this figure legend, the reader is referred to the web version of this article.)

allele frequency of 0.517, 0.516, 0.383, 0.509, and 0.397 in the AFR, AMR, EAS, EUR, and SAS super-populations, respectively [27]. It can be hypothesized that affected, or drug-exposed, individuals possess additional polymorphisms, or are enriched for those identified here, that further alter transporter function and play a role in the idiosyncratic drug response phenotype [60–63]. Also epistatic interactions between multiple *ABCB1* SNPs/INDELs have been demonstrated to influence antiepileptic drug resistance [64]. Possibly a similar phenomenon is observed in self-reported healthy individuals who have either 1) not been exposed to a drug with which the epistasis-associated phenotype is observed or 2) are expressing a low level phenotype below level of personal discomfort and reporting.

4. Conclusions

Full-gene haplotypes of four genes encoding trans-acting T-metabolism proteins, *UGT2B7*, *ABCB1*, *OPRM1*, and *COMT*, were defined and characterized using substantially more polymorphic sites than previously employed in pharmacogenetic studies. In doing so, a large number of haplotypes were observed. The data presented demonstrate significant LDs between full-gene haplotypes of *CYP2D6* and those of *UGT2B7* and *COMT*; however, the functional effects of these findings need to be determined empirically. The relatively low frequency of each

haplotype and associated diplotype may confound LD estimates simply because each haplotype was only observed in combination with one other haplotype. This study also proposed an extended *ABCB1-Block -1*, which included distal untranslated exon 1, and did not substantially increase acquired information over the truncated *Block -1* reported by Sai et al. [30,31]. Most individual haplotypes identified in this study were quite rare; however, relatively common haplotypes ($\geq 1\%$ global frequency) were identified which contain at least one damaging, or most likely damaging, polymorphism. It should be noted that copy number variation and *CYP2D6/CYP2D7* gene conversion do occur in some individuals, primary UMs and may alter the presented LD and regression patterns [65]. These events were not considered herein for determining of CYP2D6 activity [11] due to the limitations of short read sequences that comprise 1000 Genomes Project data [66,67]. It is likely that ongoing developments in longer read sequencing technologies will provide more confident interpretation of structural variation from existing short-read sequences [68–71].

The variant effects of many polymorphisms included in these haplotype definitions have not been empirically evaluated by the pharmacogenetics/pharmacogenomics community. There are obvious limitations to using an algorithmic approach to variant effect [72]; however, the predicted implications on phenotype should not be overlooked, instead they can be used to narrow the pool of potentially

causal variants/haplotypes to explore empirically. The inclusion of only self-reported healthy individuals in the 1000 Genomes Project means that additional functionally-relevant haplotypes may be selected against being represented in this dataset. This limiting factor may impact the analyses performed above. It is likely that additional polymorphisms and/or specific haplotypes may be enriched, or selected for, in affected, or T-exposed, cohorts [73–75]. As such, there potentially are additional damaging haplotypes in these affected groups that have not been observed herein so a full-gene interrogation of affected cohorts may provide greater resolution to damaging haplotype population distribution. This possibility lends support to utilizing a comprehensive genotyping approach, such as relatively long-read MPS or continuous-read nanopore technology in pharmacogenetic/pharmacogenomic interrogations [70,71,76].

Though limited to a large cohort of self-reported healthy individuals, associations between individual genes have been identified which may be clinically significant. Though slight, there is a relationship between the *CYP2D6*-inferred metabolizer phenotype and the diploidy-predicted activities of *UGT2B7*, *ABCB1*, *OPRM1*, and *COMT*. This association highlights the need for comprehensive functional evaluation of the impact of polymorphisms in all five genes, and/or combinations of two, three, or four of these genes, on drug metabolism in the same individuals. It is reasonable to hypothesize that empirical evaluation of these targets will reveal the advantage of combinatorial pharmacogenetic profiles in regards to increased patient efficacy and even assisting with medico-legal accident reconstruction [18–20]. Currently, these data remain relatively scarce in the literature. The data presented herein provide a basis to interrogate the highly polymorphic T-metabolism pathway, defining full-gene haplotypes for, and characterizing the association between, five pharmacogenes that can be utilized in clinical pharmacogenetic evaluations and post-mortem molecular autopsy using gene-targeted MPS. It is likely that these data can be expanded upon, by interrogating additional ADME gene haplotypes, for broad applicability for predicting metabolizer phenotype following exposure to other opioid drugs.

Conflicts of interest

The authors report no conflict of interest.

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Appendix A. Supplementary data

Supplementary data associated with this article can be found, in the online version, at <http://dx.doi.org/10.1016/j.fsigen.2017.11.012>.

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